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Marked Up Copy for the Claim Amendment

3. (Amended) The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides ~~has~~ comprises ~~at least 50% homology to a polypeptide having a~~ an amino acid sequence selected from the group consisting of:

- (a) an amino acid sequence selected from SEQ ID NOS: 2, 4, 6, 8 and 10;
- (b) an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, wherein the amino acid sequence has at least one conservative substitution; wherein the polypeptide comprising the amino acid sequence (b) can self-assemble to form a polymer; and
- (c) an amino acid sequence comprising a fragment of at least one amino acid residue of SEQ ID NOS: 2, 4, 6, 8 and 10, wherein the polypeptide comprising the amino acid sequence (c) can self-assemble to form a polymer as determined by analysis with a sequence comparison algorithm or by visual inspection.

4. (Amended) The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 50% homology identity to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

5. (Amended) The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 60% homology identity to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

6. (Amended) The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 70% homology identity to a polypeptide having an amino acid sequence selected from the

group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

7. (Amended) The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides ~~comprises an amino acid sequence that~~ has at least 980% ~~homology identity to a polypeptide having an amino acid~~ sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

8. (Amended) The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides ~~comprises an amino acid sequence that~~ has at least 9500% ~~homology identity to a polypeptide having an amino acid~~ sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

9. (Amended) The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides ~~comprises an amino acid sequence that~~ has at least 10 consecutive amino acids of a ~~polypeptide having an amino acid~~ sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, and 10, ~~as determined by analysis with a sequence comparison algorithm or by visual inspection.~~

10. (Amended) The drug delivery system as claimed in claim 9, wherein each of the plurality of polypeptides ~~comprises an amino acid sequence that~~ has at least 50% ~~homology identity to a polypeptide having an amino acid~~ sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

11. (Amended) The drug delivery system as claimed in claim 9, wherein each of the plurality of polypeptides ~~comprises an amino acid sequence that~~ has at least 60% ~~homology identity to a polypeptide having an amino acid~~ sequence selected from the

group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

12. (Amended) The drug delivery system as claimed in claim 9, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 70% homology/identity to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

13. (Amended) The drug delivery system as claimed in claim 9, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 80% homology/identity to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

14. (Amended) The drug delivery system as claimed in claim 9, wherein each of the plurality of polypeptides comprises an amino acid sequence that has at least 90% homology/identity to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

15. (Amended) The drug delivery system as claimed in claim 1, wherein each of the plurality of polypeptides is encoded by a nucleic acid molecule selected from the group consisting of:

(a) a nucleic acid molecule comprising a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to with the nucleic acid sequence of at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;

(b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS:

1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;

(g) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and

(h) a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS. 1, 3, 5, 7 and 9, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; sequences complementary to SEQ ID NOS. 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS. 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.

16. (Amended) The drug delivery system as claimed in claim 15, wherein each of the plurality of polypeptides is encoded by a first nucleic acid molecule, which hybridizes to a second nucleic acid molecule that has a complement of a nucleic acid sequence as set forth in SEQ ID NOS. 1, 3, 5, 7 and 9, under conditions of high stringency, wherein the conditions of high stringency are hybridization at 65°C in a hybridization buffer which comprises 3.5 times 0.15 M sodium chloride/0.015 M sodium citrate at pH 7; 0.02% Ficoll; 0.02% polyvinyl pyrrolidone; 0.02% Bovine Serum Albumin; 25 mM NaH<sub>2</sub>PO<sub>4</sub> at pH 7; 0.5% sodium dodecyl sulphate; and 2 mM ethylenediaminetetracetic acid.

17. (Amended) The drug delivery system as claimed in claim 15, wherein each of the plurality of polypeptides is encoded by a first nucleic acid molecule, which hybridizes to a second nucleic acid molecule that has a complement of a nucleic acid sequence as set forth in SEQ ID NOS. 1, 3, 5, 7 and 9, under conditions of moderate stringency.

18. (Amended) The drug delivery system as claimed in claim 15, wherein each of the plurality of polypeptides is encoded by a first nucleic acid molecule, which hybridizes to

a second nucleic acid molecule that has a complement of a nucleic acid sequence as set forth in SEQ ID NOS: 1, 3, 5, 7 and 9, under conditions of low stringency, wherein the low stringency conditions are prehybridization and hybridization at 42 degrees C in 5 times SSPE; 0.3% sodium dodecyl sulphate; 200 ug/ml sheared and denatured salmon sperm DNA; and 25% formamide, and washing with 2 times 0.15 M sodium chloride 0.015 M sodium citrate at pH 7, and 0.2% sodium dodecyl sulphate at 50 degrees C.

19. (Amended) The drug delivery system as claimed in claim 15, wherein said ~~variants have~~ nucleic acid molecule has at least about 50% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 over a ~~region subsequence~~ of at least about 200 residues.

20. (Amended) The drug delivery system as claimed in claim 15, wherein the nucleic acid molecule comprises a sequence having at least 50% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 over the entire sequence.

21. (Amended) The drug delivery system as claimed in claim 15, wherein the nucleic acid molecule comprises a sequence having at least 60% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 ~~over the entire sequence.~~

22. (Amended) The drug delivery system as claimed in claim 15, wherein the nucleic acid molecule comprises a sequence having at least 70% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 ~~over the entire sequence.~~

23. (Amended) The drug delivery system as claimed in claim 15, wherein the nucleic acid molecule comprises a sequence having at least 80% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 ~~over the entire sequence.~~

24. (Amended) The drug delivery system as claimed in claim 15, wherein the nucleic acid molecule comprises a sequence having at least 90% homology to at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 ~~over the entire sequence.~~

25. (Amended) The drug delivery system as claimed in claim 15, wherein the nucleic acid molecule comprises a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, and 9.

26. (Amended) The drug delivery system as claimed in claim 15, wherein the nucleic acid molecule comprises at least 10 consecutive bases of a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, ~~variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.~~

27. (Amended) The drug delivery system as claimed in claim 26, wherein the nucleic acid molecule comprises a sequence having at least 60% homology to the nucleic acid ~~comprising a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9.~~

28. (Amended) The drug delivery system as claimed in claim 26, wherein the nucleic acid molecule comprises a sequence having at least 70% homology to the nucleic acid ~~comprising a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9.~~

29. (Amended) The drug delivery system as claimed in claim 26, wherein the nucleic acid molecule comprises a sequence having at least 80% homology to the nucleic acid ~~comprising a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9.~~

30. (Amended) The drug delivery system as claimed in claim 26, wherein the nucleic acid molecule comprises a sequence having at least 90% homology to the nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9.

32. (Amended) A method as claimed in claim 31, wherein the polypeptide has an amino acid sequence selected from the group consisting of:

- (a) an amino acid sequence selected from SEQ ID NOS: 2, 4, 6, 8 and 10;
- (b) an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, wherein the amino acid sequence has at least one conservative substitution; wherein the polypeptide comprising the amino acid sequence (b) can self-assemble to form a polymer; and
- (c) an amino acid sequence comprising a fragment of at least one amino acid residue of SEQ ID NOS: 2, 4, 6, 8 and 10, wherein the polypeptide comprising the amino acid sequence (c) can self-assemble to form a polymer SEQ ID NOS: 2, 4, 6, 8 and 10, and sequences having at least 50% homology to a sequence selected from SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

33. (Amended) A method as claimed in claim 31, wherein the polypeptide is encoded by a nucleic acid molecule comprising a sequence selected from the group consisting of:

- (a) a nucleic acid molecule comprising a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS: 1, 3, 5, 7 and 9, over a subsequence of at least 100 residues;
- (b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS: 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS: 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;

(c) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and

(d) a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS. 1, 3, 5, 7 and 9, SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.

41. (Amended) A method of encapsulating a molecule comprising the steps of:  
providing a solution of a plurality of polypeptides having an amino acid sequence selected from the group consisting of:

(a) an amino acid sequence selected from SEQ ID NOS: 2, 4, 6, 8 and 10;

(b) an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8 and 10, wherein the amino acid sequence has at least one conservative substitution; wherein the polypeptide comprising the amino acid sequence (b) can self-assemble to form a polymer; and

(c) an amino acid sequence comprising a fragment of at least one amino acid residue of SEQ ID NOS. 2, 4, 6, 8 and 10, wherein the polypeptide comprising the amino acid sequence (c) can self-assemble to form a polymer; SEQ ID NOS: 2, 4, 6, 8 and 10; and sequences having at least 50% homology to a sequence selected from SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection; and

polymerizing the plurality of polypeptides the presence of the molecule so as to encapsulate the molecule in the polymer.



43. ~~Amended:~~ A method of encapsulating a molecule comprising the steps of:

———providing a solution of a plurality of polypeptides, wherein each polypeptide is encoded by a nucleic acid ~~molecule comprising a sequence selected from the group consisting of:~~

- (a) ~~a nucleic acid molecule comprising a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;~~
- (b) ~~a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS. 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;~~
- (c) ~~a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; or~~
- (d) ~~a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS. 1, 3, 5, 7 and 9, SEQ ID NOS. 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS. 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; sequences complementary to SEQ ID NOS. 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS. 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences, under conditions of low, moderate and high stringency; and~~

polymerizing the plurality of polypeptides the presence of the molecule so as to encapsulate the molecule in the polymer.

45. ~~Amended:~~ A method of generating a variant comprising:

obtaining a nucleic acid ~~molecule comprising a sequence~~ selected from the group consisting of:

- (a) ~~a nucleic acid molecule comprising a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;~~
- (b) ~~a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS. 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;~~
- (c) ~~a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and~~
- (d) ~~a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS. 1, 3, 5, 7 and 9; SEQ ID NOS. 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS. 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; sequences complementary to SEQ ID NOS. 1, 3, 5, 7 and 9; sequences complementary to variants having at least about 50% homology to SEQ ID NOS. 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency; and fragments comprising at least 30 consecutive nucleotides of any of the foregoing sequences; and~~

modifying said sequence by one or more steps selected from the group consisting of modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, and adding one or more nucleotides to said sequence.

60. An assay for identifying functional polypeptide fragments or variants which can self-assemble to form a polymer and are encoded by nucleic acid molecules comprising a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, a subsequence fragments of SEQ ID NOS: 1, 3, 5, 7, and 9, and a sequences having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, which retain at least one property of the polypeptides of SEQ ID NOS: 2, 4, 6, 8, and 10, and sequences having at least about 50% homology to SEQ ID NOS: 2, 4, 6, 8, and 10, over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, said assay comprising the steps of:

providing a solution of a plurality of polypeptides encoded by nucleic acid molecules comprising having a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, and 10, and sequences having at least about 50% homology to SEQ ID NOS: 2, 4, 6, 8 and 10 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, polypeptide fragments or variants encoded by SEQ ID NOS: 1, 3, 5, 7, and 9, a subsequence of SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and sequences complementary to any of the foregoing sequences, in a solution containing a template molecule and alkaline earth metal ion; and

detecting a presence of a polymer in the solution.

62. A polypeptide comprising:

a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, sequences having at least 50% homology to a sequence selected from SEQ ID NOS: 2, 4, 6, 8, and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection; and

at least one functional group selected from the group consisting of an antibody, an oligosaccharide, a polynucleotide, and a polyethylene glycol.

67. A polypeptide comprising:

an amino acid sequence encoded by a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency., and

at least one functional group selected from the group consisting of an antibody, an oligosaccharide, a polynucleotide, and a polyethylene glycol.

85. (Amended) A separation agent comprising a polymer made by self-assembly of a plurality of polypeptides each of which has at least 50% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm or by visual inspection.

86. (Amended) The separation agent as claimed in claim 85, wherein each of the plurality of polypeptides each of which has at least 60% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

87. (Amended) The separation agent as claimed in claim 85, wherein each of the plurality of polypeptides each of which has at least 70% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

88. (Amended) The separation agent as claimed in claim 85, wherein each of the plurality of polypeptides each of which has at least 80% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

89. (Amended) The separation agent as claimed in claim 85, wherein each of the plurality of polypeptides each of which has at least 90% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

90. (Amended) The separation agent as claimed in claim 85, wherein each of the plurality of polypeptides is a polypeptide each of which has ~~having~~ an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

93. (Amended) The fiber as claimed in claim 92, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

94. (Amended) A lubricant comprising:  
a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

95. (Amended) A coating composition comprising a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

96. (Amended) A biochip comprising a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 50%

homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

97. (Amended) A nanomechanical component comprising a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

98. (Amended) An optical switch comprising a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 60% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

99. (Amended) An optical waveguide comprising a polymer made by self-assembly of a plurality of polypeptides, wherein each of the plurality of polypeptides has at least 50% homology to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

100. (Amended) A computer readable medium having stored thereon a sequence of a nucleic acid sequence molecule selected from the group consisting of:

(a) a nucleic acid molecule comprising a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;

(b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS. 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;

(c) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and

a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID

~~NOS. 1, 3, 5, 7 and 9, SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.~~

101. (Amended) **A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a sequence of a nucleic acid sequence molecule selected from the group consisting of:**

- (a) a nucleic acid molecule comprising a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;
- (b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS. 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;
- (c) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and
- (d) a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS. 1, 3, 5, 7 and 9, SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences

~~complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.~~

105. (Amended) A method for comparing a first sequence to a second sequence comprising the steps of:

reading the first sequence and the second sequence through use of a computer program which compares sequences; and

determining differences between the first sequence and the second sequence with the computer program,

wherein said first sequence is a sequence of a nucleic acid sequence molecule selected from the group consisting of:

(a) a nucleic acid molecule having a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS: 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;

(b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS: 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS: 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;

(c) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and

(d) a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS: 1, 3, 5, 7 and 9, SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5,



~~and (v) over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.~~

107. (Amended) A method for identifying a feature in a particular sequence comprising the steps of:

reading the particular sequence using a computer program which identifies one or more features in a sequence; and

identifying one or more features in the particular sequence with the computer program,

wherein the particular sequence is a sequence of a nucleic acid molecule selected from the group consisting of:

(a) a nucleic acid molecule comprising a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;

(b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS. 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;

(c) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and

(d) a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS. 1, 3, 5, 7 and 9, SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS. 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection; sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that

hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.

108. (Amended) A protein preparation comprising a polypeptide having an amino acid sequence selected from the group consisting of:

- (a) an amino acid sequence selected from SEQ ID NOS. 2, 4, 6, 8 and 10;
- (b) an amino acid sequence selected from the group consisting of SEQ ID NOS. 2, 4, 6, 8 and 10, wherein the amino acid sequence has at least one conservative substitution; wherein the polypeptide comprising the amino acid sequence (b) can self-assemble to form a polymer; and
- (c) an amino acid sequence comprising a fragment of at least one amino acid residue of SEQ ID NOS. 2, 4, 6, 8 and 10, wherein the polypeptide comprising the amino acid sequence (c) can self-assemble to form a polymer~~SEQ ID NOS: 2, 4, 6, 8 and 10.~~  
sequences having at least about 50% homology to a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10, as determined by analysis with a sequence comparison algorithm, and sequences having at least 10 consecutive amino acid residues of a sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8 and 10.

109. (Amended) An expression vector capable of replicating in a host cell comprising a polynucleotide having a sequence of a nucleic acid molecule selected from the group consisting of:

- (a) a nucleic acid molecule comprising a sequence having at least 50% homology with the nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9 over a subsequence of at least 100 residues;
- (b) a nucleic acid molecule which hybridizes under low, moderate or high stringency conditions with at least one of (i) the nucleic acid sequences of SEQ ID NOS. 1, 3, 5, 7 and 9, (ii) a complementary strand of a nucleic acid sequence of at least one of SEQ ID NOS. 1, 3, 5, 7 and 9, and a subsequence thereof of at least 100 nucleotides;
- (c) a subsequence of (a) or (b), wherein the subsequence encodes a polypeptide, which can self-assemble to form a polymer; and

- (d) a nucleic acid molecule that encodes a polypeptide having an amino acid sequence that has at least 50% identity with at least one amino acid sequence of SEQ ID NOS: 1, 3, 5, 7 and 9. ~~SEQ ID NOS: 1, 3, 5, 7 and 9, variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, sequences complementary to SEQ ID NOS: 1, 3, 5, 7 and 9, and sequences complementary to variants having at least about 50% homology to SEQ ID NOS: 1, 3, 5, 7 and 9 over a region of at least about 100 residues, as determined by analysis with a sequence comparison algorithm or by visual inspection, and isolated nucleic acids that hybridize to nucleic acids having any of the foregoing sequences under conditions of low, moderate and high stringency.~~